



SEQUENCE LISTING

sub
B17

<110> Kato, Seishi
Sekine, Shingo
Kimura, Tomoko

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE
DOMAINS AND DNAS ENCODING THESE PROTEINS

<130> GIN-6706CPUS

<140> 09/445,258

<141> 1999-12-01

<150> PCT/US98/02445

<151> 1998-06-03

<150> JP 9-144948

<151> 1997-06-03

<160> 54

<170> FastSEQ for Windows Version 4.0

a2
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<211> 382

<212> PRT

<213> Homo sapiens

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Gly	Ala	Met	Ser	Pro	Pro	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu
		20						25					30		
Ser	Arg	Gly	Cys	Asn	Asp	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala
		35					40					45			
Leu	Arg	Asp	Ile	Asn	Lys	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu
	50					55				60					
Asn	Arg	Val	Asn	Asp	Ala	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser
65					70				75					80	
Leu	Phe	Tyr	Leu	Thr	Leu	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu
			85					90					95		
Arg	Lys	Lys	Ala	Trp	Gln	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser
		100						105					110		
Val	Tyr	Gly	Gln	Cys	Lys	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg
		115					120						125		
Val	Leu	Tyr	Leu	Ala	Ala	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys
	130					135					140				
Lys	Lys	Ile	Tyr	Met	Thr	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr
145					150				155					160	
Asp	Ser	Ser	Asn	His	Gln	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala
			165						170					175	
Lys	Tyr	Asn	Asn	Glu	Asn	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val
			180					185					190		

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Thr Arg Ala Ser Ser Gln Trp Val Val Gly Pro Ser Tyr Phe Val Glu
    195                200                205
Tyr Leu Ile Lys Glu Ser Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys
    210                215                220
Ser Leu Gln Ser Ser Asp Ser Val Pro Val Gly Leu Cys Lys Gly Ser
    225                230                235                240
Leu Thr Arg Thr His Trp Glu Lys Phe Val Ser Val Thr Cys Asp Phe
                245                250                255
Phe Glu Ser Gln Ala Pro Ala Thr Gly Ser Glu Asn Ser Ala Val Asn
                260                265                270
Gln Lys Pro Thr Asn Leu Pro Lys Val Glu Glu Ser Gln Gln Lys Asn
                275                280                285
Thr Pro Pro Thr Asp Ser Pro Ser Lys Ala Gly Pro Arg Gly Ser Val
    290                295                300
Gln Tyr Leu Pro Asp Leu Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro
    305                310                315                320
Gln Glu Ala Phe Pro Val His Leu Asp Leu Thr Thr Asn Pro Gln Gly
                325                330                335
Glu Thr Leu Asp Ile Ser Phe Leu Phe Leu Glu Pro Met Glu Glu Lys
    340                345                350
Leu Val Val Leu Pro Phe Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys
    355                360                365
Pro Gly Pro Ala Gln Asn Ala Ser Pro Leu Val Leu Pro Pro
    370                375                380

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<210> 2
<211> 317
<212> PRT
<213> Homo sapiens

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<400> 2
Met Trp Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His
    1                5                10                15
Trp Tyr Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val
    20                25                30
Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln
    35                40                45
Leu Asp Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys
    50                55                60
Gly Ala Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val
    65                70                75                80
Thr Leu Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp
                85                90                95
Val Lys Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn
                100                105                110
Ala Gly Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu
                115                120                125
Asp Ser Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val
    130                135                140
Thr Leu Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val
    145                150                155                160
Asn Val Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr
                165                170                175
Cys Val Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg
    180                185                190
Glu Ile Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr

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195	200	205
Phe Arg Thr Gly Met Thr	Asn Met Thr Gln Ser	Leu Glu Arg Met Lys
210	215	220
Gln Ser Trp Lys Glu Ala	Pro Lys His Ile Lys	Glu Thr Tyr Gly Gln
225	230	235
Gln Tyr Phe Asp Ala Leu	Tyr Asn Ile Met Lys	Glu Gly Leu Leu Asn
	245	250
Cys Ser Thr Asn Leu Asn	Leu Val Thr Asp Cys	Met Glu His Ala Leu
	260	265
Thr Ser Val His Pro Arg	Thr Arg Tyr Ser Ala	Gly Trp Asp Ala Lys
	275	280
Phe Phe Phe Ile Pro Leu	Ser Tyr Leu Pro Thr	Ser Leu Ala Asp Tyr
	290	295
Ile Leu Thr Arg Ser Trp	Pro Lys Pro Ala Gln	Ala Val
305	310	315

<210> 3
 <211> 296
 <212> PRT
 <213> Homo sapiens

<400> 3

Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly	
1 5 10 15	
Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu	
20 25 30	
Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro	
35 40 45	
Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn	
50 55 60	
Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys	
65 70 75 80	
Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly	
85 90 95	
Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
100 105 110	
Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
115 120 125	
Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu	
130 135 140	
Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
145 150 155 160	
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	
165 170 175	
Tyr Gln Glu Leu Thr Glu Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
180 185 190	
Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala	
195 200 205	
Ala Val Gly Glu Leu Pro Asp Gln Ser Lys Gln Gln Gln Ile Tyr Gln	
210 215 220	
Glu Leu Thr Asp Leu Lys Thr Ala Phe Glu Arg Leu Cys Arg His Cys	
225 230 235 240	
Pro Lys Asp Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn	
245 250 255	
Ser Gln Arg Asn Trp His Asp Ser Val Thr Ala Cys Gln Glu Val Arg	
260 265 270	

Ala Gln Leu Val Val Ile Lys Thr Ala Glu Glu Gln Leu Pro Ala Val
 275 280 285
 Leu Glu Gln Trp Arg Thr Gln Gln
 290 295

<210> 4
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Cys Thr Gly Lys Cys Ala Arg Cys Val Gly Leu Ser Leu Ile Thr
 1 5 10 15
 Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn
 20 25 30
 Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp
 35 40 45
 Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly
 50 55 60
 Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys
 65 70 75 80
 Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe
 85 90 95
 Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu
 100 105 110
 Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe
 115 120 125
 Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg
 130 135 140
 Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser
 145 150 155 160
 Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln
 165 170 175
 Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys
 180 185 190
 Gln Asp Thr Pro His
 195

<210> 5
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
 1 5 10 15
 Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
 20 25 30
 Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
 35 40 45
 Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
 50 55 60
 Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
 65 70 75 80
 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val

			85					90				95			
Val	Leu	Leu	Gln	Thr	Ala	Thr	Leu	Leu	Gly	Val	Leu	Leu	Leu	Gly	Tyr
			100					105					110		
Gly	Tyr	Phe	Trp	Leu	Leu	Val	Pro	Asn	Pro	Glu	Ala	Arg	Leu	Gln	Gln
		115					120					125			
Leu	Gly	Leu	Phe	Cys	Ser	Val	Phe	Thr	Ile	Ser	Met	Tyr	Leu	Ser	Pro
	130					135					140				
Leu	Ala	Asp	Leu	Ala	Lys	Val	Ile	Gln	Thr	Lys	Ser	Thr	Gln	Cys	Leu
145					150					155					160
Ser	Tyr	Pro	Leu	Thr	Ile	Ala	Thr	Leu	Leu	Thr	Ser	Ala	Ser	Trp	Cys
			165						170					175	
Leu	Tyr	Gly	Phe	Arg	Leu	Arg	Asp	Pro	Tyr	Ile	Met	Val	Ser	Asn	Phe
		180						185					190		
Pro	Gly	Ile	Val	Thr	Ser	Phe	Ile	Arg	Phe	Trp	Leu	Phe	Trp	Lys	Tyr
		195					200					205			
Pro	Gln	Glu	Gln	Asp	Arg	Asn	Tyr	Trp	Leu	Leu	Gln	Thr			
	210					215					220				

<210> 6

<211> 251

<212> PRT

<213> Homo sapiens

<400> 6

Met	Ser	Asp	Ile	Gly	Asp	Trp	Phe	Arg	Ser	Ile	Pro	Ala	Ile	Thr	Arg
1				5					10					15	
Tyr	Trp	Phe	Ala	Ala	Thr	Val	Ala	Val	Pro	Leu	Val	Gly	Lys	Leu	Gly
		20					25					30			
Leu	Ile	Ser	Pro	Ala	Tyr	Leu	Phe	Leu	Trp	Pro	Glu	Ala	Phe	Leu	Tyr
	35					40					45				
Arg	Phe	Gln	Ile	Trp	Arg	Pro	Ile	Thr	Ala	Thr	Phe	Tyr	Phe	Pro	Val
	50				55					60					
Gly	Pro	Gly	Thr	Gly	Phe	Leu	Tyr	Leu	Val	Asn	Leu	Tyr	Phe	Leu	Tyr
65				70					75					80	
Gln	Tyr	Ser	Thr	Arg	Leu	Glu	Thr	Gly	Ala	Phe	Asp	Gly	Arg	Pro	Ala
			85					90					95		
Asp	Tyr	Leu	Phe	Met	Leu	Leu	Phe	Asn	Trp	Ile	Cys	Ile	Val	Ile	Thr
		100					105					110			
Gly	Leu	Ala	Met	Asp	Met	Gln	Leu	Leu	Met	Ile	Pro	Leu	Ile	Met	Ser
	115					120						125			
Leu	Leu	Tyr	Val	Trp	Ala	Gln	Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe
	130					135					140				
Trp	Phe	Gly	Thr	Arg	Phe	Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu
145				150					155					160	
Gly	Phe	Asn	Tyr	Ile	Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly
		165						170						175	
Asn	Leu	Val	Gly	His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met
		180					185						190		
Asp	Leu	Gly	Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg
	195					200						205			
Trp	Leu	Pro	Ser	Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro
	210					215						220			
Ala	Ser	Met	Arg	Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His
225					230					235				240	
Asn	Trp	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Asp	Gln					
			245					250							

<210> 7
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro Ser
 1 5 10 15
 Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn Pro
 20 25 30
 Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro Val
 35 40 45
 Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Leu Thr Tyr Gly Leu
 50 55 60
 Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met Arg
 65 70 75 80
 Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu Gly
 85 90 95
 Leu Ala Val Thr Ala Met Lys Ser Arg Pro
 100 105

<210> 8
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser
 1 5 10 15
 Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu
 20 25 30
 Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu
 35 40 45
 Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
 50 55 60
 Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
 65 70 75

<210> 9
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
 1 5 10 15
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
 20 25 30
 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala
 35 40 45
 Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro
 50 55 60
 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala

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65          70          75          80
Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val
      85          90          95
Ile Leu Ala Gln Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His
      100          105          110
Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys
      115          120          125
Gln Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu
      130          135          140
Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu
      145          150          155
Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys
      165          170          175
Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu
      180          185          190
Lys Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr
      195          200          205
Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
      210          215          220
Gln Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu
      225          230          235
Arg Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly
      245          250          255
Thr Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr
      260          265          270
Pro Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg
      275          280          285
Val Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp
      290          295          300
Gly Arg Glu Ser Pro Ala Gln Ala Pro Ala
305          310

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<210> 10
<211> 195
<212> PRT
<213> Homo sapiens

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<400> 10
Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
 1          5          10          15
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
      20          25          30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
      35          40          45
Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Glu Pro Pro Pro
      50          55          60
Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
      65          70          75          80
Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
      85          90          95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
      100          105          110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
      115          120          125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
      130          135          140

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Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
 145 150 155 160
 Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
 165 170 175
 Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg
 180 185 190
 Lys Asn Asp
 195

<210> 11
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
 1 5 10 15
 Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
 20 25 30
 Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
 35 40 45
 Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu His Glu Arg
 50 55 60
 Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser
 65 70 75 80
 Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro Asn Lys Thr
 85 90 95
 Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg Tyr Gln Ser
 100 105 110
 Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys Leu Tyr Glu
 115 120 125
 Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu Leu Leu Lys
 130 135 140
 Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln
 145 150 155 160
 His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met Lys Ser Val
 165 170 175
 Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile
 180 185 190
 Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly
 195 200 205
 Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr
 210 215 220
 Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys
 225 230 235 240
 Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser Leu
 245 250 255
 Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser Met Ile
 260 265 270
 Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys Thr Trp Ala
 275 280 285
 Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys Lys Leu Tyr Glu
 290 295 300
 Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val Thr Pro Glu Lys Ile
 305 310 315 320
 Glu Gln Leu Arg Tyr Cys Gln His Val Leu Cys Glu Thr Val Arg Thr


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<210> 12
<211> 247
<212> PRT
<213> Homo sapiens
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[illegible]

<210> 13
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
 1 5 10 15
 Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
 20 25 30
 Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
 35 40 45
 Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
 50 55 60
 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
 65 70 75 80
 Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
 85 90 95
 Thr Leu Leu Ser Lys Gly Phe Arg Gly Pro Ser Pro His Arg Lys Ser
 100 105 110
 Thr

<210> 14
 <211> 365
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu
 1 5 10 15
 Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr
 20 25 30
 Phe Tyr Asn Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met
 35 40 45
 Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg
 50 55 60
 Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp
 65 70 75 80
 Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala Leu
 85 90 95
 Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser Leu
 100 105 110
 Tyr Thr Met Thr Lys Ser Ser Ala Val Leu Phe Ile Leu Ile Phe Ser
 115 120 125
 Leu Ile Phe Lys Leu Glu Glu Leu Arg Ala Ala Leu Val Leu Val Val
 130 135 140
 Leu Leu Ile Ala Gly Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln
 145 150 155 160
 Phe Asn Val Glu Gly Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly
 165 170 175
 Gly Ile Arg Trp Thr Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu
 180 185 190
 Gly Leu Gln Asn Pro Ile Asp Thr Met Phe His Leu Gln Pro Leu Met

195	200	205
Phe Leu Gly Leu Phe Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu		
210	215	220
Ser Thr Ser Glu Lys Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu		
225	230	235
Arg Val Leu Gly Ser Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu		
245	250	255
Gly Phe Ser Glu Phe Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu		
260	265	270
Ser Ile Ala Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala		
275	280	285
His Leu Leu Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala		
290	295	300
Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His		
305	310	315
Ser Arg Gly Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser		
325	330	335
Pro Asp Leu Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp		
340	345	350
Asn Glu Glu Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln		
355	360	365

<210> 15

<211> 226

<212> PRT

<213> Homo sapiens

<400> 15

Met Pro Thr Thr Lys Lys Thr Leu Met Phe Leu Ser Ser Phe Phe Thr	
1	5
Ser Leu Gly Ser Phe Ile Val Ile Cys Ser Ile Leu Gly Thr Gln Ala	
20	25
Trp Ile Thr Ser Thr Ile Ala Val Arg Asp Ser Ala Ser Asn Gly Ser	
35	40
Ile Phe Ile Thr Tyr Gly Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu	
50	55
Ser His Gly Leu Ala Glu Pro Lys Lys Lys Phe Ala Val Leu Glu Ile	
65	70
Leu Asn Asn Ser Ser Gln Lys Thr Leu His Ser Val Thr Ile Leu Phe	
85	90
Leu Val Leu Ser Leu Ile Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe	
100	105
Tyr Asn Ser Ile Ser Asn Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly	
115	120
Val Tyr Thr Trp Asn Gly Leu Gly Ala Ser Phe Val Phe Val Thr Met	
130	135
Ile Leu Phe Val Ala Asn Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu	
145	150
Phe Gln Met Leu Tyr Pro Ala Thr Thr Ser Lys Gly Thr Thr His Ser	
165	170
Tyr Gly Tyr Ser Phe Trp Leu Ile Leu Leu Val Ile Leu Leu Asn Ile	
180	185
Val Thr Val Thr Ile Ile Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg	
195	200
Lys Gln Glu Gln Arg Lys Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile	
210	215
	220

Leu Phe
225

<210> 16
<211> 129
<212> PRT
<213> Homo sapiens

<400> 16
Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
1 5 10 15
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
20 25 30
Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
35 40 45
Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
50 55 60
Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65 70 75 80
Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
85 90 95
Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
100 105 110
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115 120 125
Gln

<210> 17
<211> 163
<212> PRT
<213> Homo sapiens

<400> 17
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Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln
35 40 45
Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile
50 55 60
Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg
65 70 75 80
Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg
85 90 95
Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly
100 105 110
Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu
115 120 125
Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp
130 135 140
Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu
145 150 155 160
Pro Arg Ser

<210> 18
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 18
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 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
 35 40 45
 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
 50 55 60
 Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
 65 70 75 80
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 85 90 95
 Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
 100 105 110
 Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile
 115 120 125
 Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Arg Ala
 130 135 140
 Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
 145 150 155 160
 Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
 165 170 175
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<210> 19
 <211> 1146
 <212> DNA
 <213> Homo sapiens

<400> 19
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<210> 20

<211> 951

<212> DNA

<213> Homo sapiens

<400> 20

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tttgggaacc tgctggccag acagctggat gcacgaggct tgagagtgtt ggctgcgtgt 180
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aatgtctcca gcattctggg aagagttgct ttctttgtag gaggctactg tgtctccaag 540
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<210> 21

<211> 888

<212> DNA

<213> Homo sapiens

<400> 21

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tggcacgact ccgtcaccgc ctgccaggaa gtgagggccc agctcgtcgt aatcaaaact 840
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<210> 22

<211> 591

<212> DNA

<213> Homo sapiens

<400> 22

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aaccatctca gcttgcaagt ctggctcatg ggcggcttca ttggcggggg cctaattgga 180
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<210> 23

<211> 663

<212> DNA

<213> Homo sapiens

<400> 23

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cgactcagag atccctatat catggtgtcc aactttccag gaatcgtcac cagctttatc 600
cgcttctggc ttttctggaa gtacccccag gagcaagaca ggaactactg gctcctgcaa 660
acc 663

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<210> 24

<211> 753

<212> DNA

<213> Homo sapiens

<400> 24

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atgctcctct ttaactgat ttgcatcgtg attactggct tagcaatgga tatgcagttg 360
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tccacacctc agtttttcta ccgctggctg cccagtagga gaggaggagt atcaggattt 660
ggtgtgcccc ctgctagcat gaggcgagct gctgatcaga atggcggagg cgggagacac 720
aactggggcc agggctttcg acttgagagc cag 753

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<210> 25

<211> 318

<212> DNA

<213> Homo sapiens

<400> 25

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attgaggggc tgagccccac tgtttacagg aatccagaga gtttcaagga aaagttcggt 120
cgcaagaccc gcgagaaccc ggtggtaccc ataggttgcc tggccacggc ggccgccctc 180
acctacggcc tctactcctt ccaccggggc aacagccagc gctctcagct catgatgcgc 240
acccggatcg ccgcccaggg ttccacggtc gcagccatct tgctgggtct ggctgtcact 300
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<210> 26

<211> 234

<212> DNA

<213> Homo sapiens

<400> 26

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gagtcagctt tcttgaattt gcttgaaaag ctctgcctcc tctccatct cccttcaggg 180
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<210> 27

<211> 942

<212> DNA

<213> Homo sapiens

<400> 27

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aacttcattc gacagcgggg ccgggtgtcc atcgccgagc ttgcccgaag cagcaactcc 900
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<210> 28

<211> 585

<212> DNA

<213> Homo sapiens

<400> 28

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gagccgcccc ctctgcccc cctcaagcgg cgcgacttca cccccccga gctgcggcgc 240
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gacctttctg acctcactgc tgcccagcag gagactctga gtgactggga gtctcagttc 480
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<210> 29
 <211> 1386
 <212> DNA
 <213> Homo sapiens

<400> 29
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<210> 30
 <211> 741
 <212> DNA
 <213> Homo sapiens

<400> 30
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<210> 31
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 31

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<210> 32

<211> 1095

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33

<211> 678

<212> DNA

<213> Homo sapiens

<400> 33

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taccagaagg ccagatacca gcggaagcag gagcagagaa agccaatgga atatgctcca 660
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<210> 34

<211> 387

<212> DNA

<213> Homo sapiens

<400> 34

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tcctggagcg cggacctgga caagtgcctg gactgcgcgt cttgcaggcg gcgaccgcac 180
agcgacttct gctggggctg cgctgcagca cctcctgccc cttccggct gctttggccc 240
atccttgggg gcgctctgag cctgaccttc gtgctggggc tgctttctgg ctttttggtc 300
tgagacgat gccgcaggag agagaagttc accaccccca tagaggagac cggcggagag 360
ggctgcccag ctgtggcgct gatccag                                     387

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<210> 35

<211> 489

<212> DNA

<213> Homo sapiens

<400> 35

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ccgcccgtgc agtgggcctt ccaggagacc agtgtggaga gcgccgtgga cagcccttc 180
ccagctgga tatttgtgag gctggaattt aagctgcagc agacaagctg ccggaagagg 240
gactggaaga aaccogagtg caaagtcagg cccaatggga ggaaacggaa atgcctggcc 300
tgcataaaac tgggctctga ggacaaagtt ctgggccggg tggccactg ccccatagag 360
acccaagttc tgcgggaggc tgaggagcac caggagaccc agtgccctcag ggtgcagcgg 420
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<210> 36

<211> 579

<212> DNA

<213> Homo sapiens

<400> 36'

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agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggttgca gtctagcgac 120
cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180
tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
ctcttctgtg gcttcatcat cctggtgate tgtttcatcc tctccttctt cgccctctgt 300
ggaccccaga tgcttgtctt cctgagagtg attggaggtc tccttgccct ggctgctgtg 360
ttccagatca tctccctggg aatttaccoc gtgaagtaca ccagacctt cacccttcat 420
gccaacctg ctgtcaacta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga tcggctgtgc cttcttcttc tgctgcctcc ccaactacga agatgacctt 540
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<210> 37

<211> 1502

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (37)...(1185)

<400> 37

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Met Gly Leu Leu Leu Pro
1 5

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ctg gca ctc tgc atc cta gtc ctg tgc tgc gga gca atg tct cca ccc	102
Leu Ala Leu Cys Ile Leu Val Leu Cys Cys Gly Ala Met Ser Pro Pro	
10 15 20	
cag ctg gcc ctc aac ccc tcg gct ctg ctc tcc cgg ggc tgc aat gac	150
Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu Ser Arg Gly Cys Asn Asp	
25 30 35	
tcc gat gtg ctg gca gtt gca ggc ttt gcc ctg cgg gat att aac aaa	198
Ser Asp Val Leu Ala Val Ala Gly Phe Ala Leu Arg Asp Ile Asn Lys	
40 45 50	
gac aga aag gat ggc tat gtg ctg aga ctc aac cga gtg aac gac gcc	246
Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu Asn Arg Val Asn Asp Ala	
55 60 65 70	
cag gaa tac aga cgg ggt ggc ctg gga tct ctg ttc tat ctt aca ctg	294
Gln Glu Tyr Arg Arg Gly Gly Leu Gly Ser Leu Phe Tyr Leu Thr Leu	
75 80 85	
gat gtg cta gag act gac tgc cat gtg ctc aga aag aag gca tgg caa	342
Asp Val Leu Glu Thr Asp Cys His Val Leu Arg Lys Lys Ala Trp Gln	
90 95 100	
gac tgt gga atg agg ata ttt ttt gaa tca gtt tat ggt caa tgc aaa	390
Asp Cys Gly Met Arg Ile Phe Phe Glu Ser Val Tyr Gly Gln Cys Lys	
105 110 115	
gca ata ttt tat atg aac aac cca agt aga gtt ctc tat tta gct gct	438
Ala Ile Phe Tyr Met Asn Asn Pro Ser Arg Val Leu Tyr Leu Ala Ala	
120 125 130	
tat aac tgt act ctt cgc cca gtt tca aaa aaa aag att tac atg acg	486
Tyr Asn Cys Thr Leu Arg Pro Val Ser Lys Lys Lys Ile Tyr Met Thr	
135 140 145 150	
tgc cct gac tgc cca agc tcc ata ccc act gac tct tcc aat cac caa	534
Cys Pro Asp Cys Pro Ser Ser Ile Pro Thr Asp Ser Ser Asn His Gln	
155 160 165	
gtg ctg gag gct gcc acc gag tct ctt gcg aaa tac aac aat gag aac	582
Val Leu Glu Ala Ala Thr Glu Ser Leu Ala Lys Tyr Asn Asn Glu Asn	
170 175 180	
aca tcc aag cag tat tct ctc ttc aaa gtc acc agg gct tct agc cag	630
Thr Ser Lys Gln Tyr Ser Leu Phe Lys Val Thr Arg Ala Ser Ser Gln	
185 190 195	
tgg gtg gtc ggc cct tct tac ttt gtg gaa tac tta att aaa gaa tca	678
Trp Val Val Gly Pro Ser Tyr Phe Val Glu Tyr Leu Ile Lys Glu Ser	
200 205 210	
cca tgt act aaa tcc cag gcc agc agc tgt tca ctt cag tcc tcc gac	726
Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys Ser Leu Gln Ser Ser Asp	
215 220 225 230	
tct gtg cct gtt ggt ctt tgc aaa ggt tct ctg act cga aca cac tgg	774

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Ser Val Pro Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp
                235                      240                      245

gaa aag ttt gtc tct gtg act tgt gac ttc ttt gaa tca cag gct cca 822
Glu Lys Phe Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro
                250                      255                      260

gcc act gga agt gaa aac tct gct gtt aac cag aaa cct aca aac ctt 870
Ala Thr Gly Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu
                265                      270                      275

ccc aag gtg gaa gaa tcc cag cag aaa aac acc ccc cca aca gac tcc 918
Pro Lys Val Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser
                280                      285                      290

ccc tcc aaa gct ggg cca aga gga tct gtc caa tat ctt cct gac ttg 966
Pro Ser Lys Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu
295                      300                      305                      310

gat gat aaa aat tcc cag gaa aag ggc cct cag gag gcc ttt cct gtg 1014
Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val
                315                      320                      325

cat ctg gac cta acc acg aat ccc cag gga gaa acc ctg gat att tcc 1062
His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser
                330                      335                      340

ttc ctc ttc ctg gag cct atg gag gag aag ctg gtt gtc ctg cct ttc 1110
Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe
                345                      350                      355

ccc aaa gaa aaa gca cgc act gct gag tgc cca ggg cca gcc cag aat 1158
Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn
                360                      365                      370

gcc agc cct ctt gtc ctt ccg cca tga gaatcacaca gagtcttctg 1205
Ala Ser Pro Leu Val Leu Pro Pro *
375                      380

taggggtatg gtgcgccgca tgacatggga ggcgatgggg acgatggaca gagacagagc 1265
gtgcacacgt agagtggcta gtgaaggacg cctttttgac tcttcttggt ctgagcatgt 1325
tgactgggat tggaaataat gagactgagc cctcggtctg ggctgcactc taccctgtac 1385
actgccttgt accctgagct gcatcacctc ctaaaactgag cagtctcata ccatggagag 1445
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<211> 1349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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tctaggactg gactcttctt aagcaagtcc gagaaggaag caccctcact atg tgg 116

```

Met Trp
1

ctc tac ctg gcg gcc ttc gtg ggc ctg tac tac ctt ctg cac tgg tac	164
Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr	
5 10 15	
cgg gag agg cag gtg gtg agc cac ctc caa gac aag tat gtc ttt atc	212
Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile	
20 25 30	
acg ggc tgt gac tcg ggc ttt ggg aac ctg ctg gcc aga cag ctg gat	260
Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp	
35 40 45 50	
gca cga ggc ttg aga gtg ctg gct gcg tgt ctg acg gag aag ggg gcc	308
Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala	
55 60 65	
gag cag ctg agg ggc cag acg tct gac agg ctg gag acg gtg acc ctg	356
Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu	
70 75 80	
gat gtt acc aag atg gag agc atc gct gca gct act cag tgg gtg aag	404
Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys	
85 90 95	
gag cat gtg ggg gac aga gga ctc tgg gga ctg gtg aac aat gca ggc	452
Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn Ala Gly	
100 105 110	
att ctt aca cca att acc tta tgt gag tgg ctg aac act gag gac tct	500
Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu Asp Ser	
115 120 125 130	
atg aat atg ctc aaa gtg aac ctc att ggt gtg atc cag gtg acc ttg	548
Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val Thr Leu	
135 140 145	
agc atg ctt cct ttg gtg agg aga gca cgg gga aga att gtc aat gtc	596
Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val Asn Val	
150 155 160	
tcc agc att ctg gga aga gtt gct ttc ttt gta gga ggc tac tgt gtc	644
Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr Cys Val	
165 170 175	
tcc aag tat gga gtg gaa gcc ttt tca gat att ctg agg cgt gag att	692
Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg Glu Ile	
180 185 190	
caa cat ttt ggg gtg aaa atc agc ata gtt gaa cct ggc tac ttc aga	740
Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr Phe Arg	
195 200 205 210	
acg gga atg aca aac atg aca cag tcc tta gag cga atg aag caa agt	788
Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys Gln Ser	

215	220	225	
tgg aaa gaa gcc ccc aag cat att aag gag acc tat gga cag cag tat			836
Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln Gln Tyr			
230	235	240	
ttt gat gcc ctt tac aat atc atg aag gaa ggg ctg ttg aat tgt agc			884
Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn Cys Ser			
245	250	255	
aca aac ctg aac ctg gtc act gac tgc atg gaa cat gct ctg aca tcg			932
Thr Asn Leu Asn Leu Val Thr Asp Cys Met Glu His Ala Leu Thr Ser			
260	265	270	
gtg cat ccg cga act cga tat tca gct ggc tgg gat gct aaa ttt ttc			980
Val His Pro Arg Thr Arg Tyr Ser Ala Gly Trp Asp Ala Lys Phe Phe			
275	280	285	290
ttc atc cct cta tct tat tta cct aca tca ctg gca gac tac att ttg			1028
Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr Ile Leu			
295	300	305	
act aga tct tgg ccc aaa cca gcc cag gca gtc taa agaaaaactgg			1074
Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val *			
310	315		
gttggtgctt cttggaatga aggcaaaaat ctgaaattgt tagtgtctca gtaatcctga 1134			
tttagaaccc aggctttttg taacaatgtg ttttcttgcc taaattcatt tatctggcat 1194			
catcagagta ctaacatgtt tatatttcag atatccaaag cttaccactt taggtgatga 1254			
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	Met Ser Asp Ser Lys Glu Pro Arg Val		
	1 5		
cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg			99
Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu			
10 15 20 25			
caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt			147
Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu			
30 35 40			
gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag			195
Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu			
45 50 55			

caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt	243
Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly	
60 65 70	
gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc	291
Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
75 80 85	
cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag	339
Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
90 95 100 105	
gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg	387
Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu	
110 115 120	
cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg	435
Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
125 130 135	
aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc	483
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	
140 145 150	
tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag	531
Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
155 160 165	
aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct	579
Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala	
170 175 180 185	
gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag	627
Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln	
190 195 200	
gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc	675
Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser	
205 210 215	
aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt	723
Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe	
220 225 230	
gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga	771
Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly	
235 240 245	
aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc gtc	819
Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val	
250 255 260 265	
acc gcc tgc cag gaa gtg agg gcc cag ctc gtc gta atc aaa act gct	867
Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala	
270 275 280	


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Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu Arg Asn Gly Pro Arg Cys
    105                      110                      115

tta atg aac ggc gag tgg ggc tac cac ttc gaa gac acc gcg gga gct 439
Leu Met Asn Gly Glu Trp Gly Tyr His Phe Glu Asp Thr Ala Gly Ala
    120                      125                      130

tac ttg ctc aac cgc act cta tgg gat cgg tgc gag gcg ccc cct cgc 487
Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg Cys Glu Ala Pro Pro Arg
    135                      140                      145                      150

gtg gtc ccc tgg aat gtg acg ctc ttc tcg ctg ctg gtg gcc gcc tcc 535
Val Val Pro Trp Asn Val Thr Leu Phe Ser Leu Leu Val Ala Ala Ser
    155                      160                      165

tgc ctg gag ata gta ctg tgt ggg atc cag ctg gtg aac gcg acc att 583
Cys Leu Glu Ile Val Leu Cys Gly Ile Gln Leu Val Asn Ala Thr Ile
    170                      175                      180

ggg gtc ttc tgc ggc gat tgc agg aaa aaa cag gac acc cct cac tga 631
Gly Val Phe Cys Gly Asp Cys Arg Lys Lys Gln Asp Thr Pro His *
    185                      190                      195

ggctccactg accgcccggg tacacctgct ccttcctgga cgcctacctg gctcgctcac 691
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<210> 41
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<220>
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<222> (84)...(749)

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cgcgggatcc gactctagtc gta atg gag gcg ggc ggc ttt ctg gac tcg ctc 113
                Met Glu Ala Gly Gly Phe Leu Asp Ser Leu
                  1                      5                      10

att tac gga gca tgc gtg gtc ttc acc ctt ggc atg ttc tcc gcc ggc 161
Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly
    15                      20                      25

ctc tcg gac ctc agg cac atg cga atg acc cgg agt gtg gac aac gtc 209
Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val
    30                      35                      40

cag ttc ctg ccc ttt ctc acc acg gaa gtc aac aac ctg ggc tgg ctg 257
Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu
    45                      50                      55

agt tat ggg gct ttg aag gga gac ggg atc ctc atc gtc gtc aac aca 305
Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr
    60                      65                      70

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gtg ggt gct gcg ctt cag acc ctg tat atc ttg gca tat ctg cat tac 353
 Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr
 75 80 85 90

tgc cct cgg aag cgt gtt gtg ctc cta cag act gca acc ctg cta ggg 401
 Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly
 95 100 105

gtc ctt ctc ctg ggt tat ggc tac ttt tgg ctc ctg gta ccc aac cct 449
 Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro
 110 115 120

gag gcc cgg ctt cag cag ttg ggc ctc ttc tgc agt gtc ttc acc atc 497
 Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile
 125 130 135

agc atg tac ctc tca cca ctg gct gac ttg gct aag gtg att caa act 545
 Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr
 140 145 150

aaa tca acc caa tgt ctc tcc tac cca ctc acc att gct acc ctt ctc 593
 Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu
 155 160 165 170

acc tct gcc tcc tgg tgc ctc tat ggg ttt cga ctc aga gat ccc tat 641
 Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr
 175 180 185

atc atg gtg tcc aac ttt cca gga atc gtc acc agc ttt atc cgc ttc 689
 Ile Met Val Ser Asn Phe Pro Gly Ile Val Thr Ser Phe Ile Arg Phe
 190 195 200

tgg ctt ttc tgg aag tac ccc cag gag caa gac agg aac tac tgg ctc 737
 Trp Leu Phe Trp Lys Tyr Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu
 205 210 215

ctg caa acc tga ggctgctcat ctgaccactg ggcaccttag tgccaacctg 789
 Leu Gln Thr *
 220

aaccaaagag acctccttgt ttcagctggg cctgctgtcc agcttcccag gtgcagtggg 849
 ttgtgggaac aagagatgac tttgaggata aaaggaccaa agaaaaagct ttacttagat 909
 gattgattgg ggccataggag atgaaatcac tttttatatt ttagagattt ttttttttaa 969
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 tgaaccacag aggtggagggt tgcagtgagc tgagatcgtg ccattgtgat atgaatatgc 1269
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<211> 3045

<212> DNA

<213> Homo sapiens

<220>

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<222> (191)...(946)

<400> 42

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gccgcgtcgt gagggggtcg gcacggggag tcgggcggtc ttgtgcatct tggctacctg 180
tgggtcgaag atg tcg gac atc gga gac tgg ttc agg agc atc ccg gcg 229
      Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala
        1             5             10

atc acg cgc tat tgg ttc gcc gcc acc gtc gcc gtg ccc ttg gtc ggc 277
Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly
      15             20             25

aaa ctc ggc ctc atc agc ccg gcc tac ctc ttc ctc tgg ccc gaa gcc 325
Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
      30             35             40             45

ttc ctt tat cgc ttt cag att tgg agg cca atc act gcc acc ttt tat 373
Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr
              50             55             60

ttc cct gtg ggt cca gga act gga ttt ctt tat ttg gtc aat tta tat 421
Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr
              65             70             75

ttc tta tat cag tat tct acg cga ctt gaa aca gga gct ttt gat ggg 469
Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly
              80             85             90

agg cca gca gac tat tta ttc atg ctc ctc ttt aac tgg att tgc atc 517
Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile
              95             100             105

gtg att act ggc tta gca atg gat atg cag ttg ctg atg att cct ctg 565
Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu
      110             115             120             125

atc atg tca cta ctt tat gtc tgg gcc cag ctg aac aga gac atg att 613
Ile Met Ser Leu Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile
              130             135             140

gta tca ttt tgg ttt gga aca cga ttt aag gcc tgc tat tta ccc tgg 661
Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp
              145             150             155

gtt atc ctt gga ttc aac tat atc atc gga ggc tcg gta atc aat gag 709
Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu
              160             165             170

ctt att gga aat ctg gtt gga cat ctt tat ttt ttc cta atg ttc aga 757
Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg
              175             180             185

tac cca atg gac ttg gga gga aga aat ttt cta tcc aca cct cag ttt 805
Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe
      190             195             200             205

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ttg tac cgc tgg ctg ccc agt agg aga gga gga gta tca gga ttt ggt 853
 Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly
 210 215 220

gtg ccc cct gct agc atg agg cga gct gct gat cag aat ggc gga ggc 901
 Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly
 225 230 235

ggg aga cac aac tgg ggc cag ggc ttt cga ctt gga gac cag tga 946
 Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln *
 240 245 250

aggggcggcc tcgggcagcc gctcctctca agccacattt cctcccagtg ctgggtgcgc 1006
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 ctggagtagt tgggttgctt tgtgttagga ggatccagat catgttggct acaggagat 1846
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 gtttctggaa taattttacc aaaacaagct atttgagttt tgacttgaca aggcaaaaca 2926
 tgacagtgga ttctctttac aaattgaaaa aaataatcct tattttgtat aaaggacttc 2986
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<211> 653

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63)...(383)

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 Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro
 1 5 10 15

tcg aag cct cca gtc att gag ggg ctg agc ccc act gtt tac agg aat 155
 Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn
 20 25 30

cca gag agt ttc aag gaa aag ttc gtt cgc aag acc cgc gag aac ccg 203
 Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro
 35 40 45

gtg gta ccc ata ggt tgc ctg gcc acg gcg gcc gcc ctc acc tac ggc 251
 Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly
 50 55 60

ctc tac tcc ttc cac cgg ggc aac agc cag cgc tct cag ctc atg atg 299
 Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met
 65 70 75

cgc acc cgg atc gcc gcc cag ggt ttc acg gtc gca gcc atc ttg ctg 347
 Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu
 80 85 90 95

ggt ctg gct gtc act gct atg aag tct cga ccc taa gccagggtc 393
 Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro *
 100 105

tggccttgaa agctccgcag aaatgattcc aaaacccagg gagcaaccac tggccctacc 453
 gtgggactta ctccctctc tcctttgaga ggcccatgtg tcgctgggga ggaagtgacc 513
 ctttgtgtaa ctgtaaccga aagttttttc aaaaatccta gatgctgttg tttgaatgtt 573
 acatacttct atttgtgcca catctccct ccactccct gcttaataaa ctctaaaaat 633
 ccacttgat ttaattcagt 653

<210> 44

<211> 439

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(311)

<400> 44

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 gcgcagtggc cact atg ggg tct ggg ctg ccc ctt gtc ctc ctc ttg acc 110
 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr
 1 5 10

ctc ctt ggc agc tca cat gga aca ggg ccg ggt atg act ttg caa ctg 158
 Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu
 15 20 25

aag ctg aag gag tct ttt ctg aca aat tcc tcc tat gag tcc agc ttc 206

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Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
  30                      35                      40

ctg gaa ttg ctt gaa aag ctc tgc ctc ctc ctc cat ctc cct tca ggg 254
Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
  45                      50                      55                      60

acc agc gtc acc ctc cac cat gca aga tct caa cac cat gtt gtc tgc 302
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys
                      65                      70                      75

aac aca tga cagccattga agcctgtgtc cttcttggcc cgggcttttg 351
Asn Thr *

ggccgggggat gcaggaggca ggccccgacc ctgtcttttca gcaggccccc accctcctga 411
gtggcaataa ataaaattcg gtatgctg 439

<210> 45
<211> 1131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)...(1000)

<400> 45
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                                         1

gtg gcg cct gtg tgg tac ttg gta gcg gcg gct ctg cta gtc ggc ttt 106
Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe
                      5                      10                      15

atc ctc ttc ctg act cgc agc cgg ggc cgg gcg gca tca gcc ggc caa 154
Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln
                      20                      25                      30

gag cca ctg cac aat gag gag ctg gca gga gca ggc cgg gtg gcc cag 202
Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln
                      35                      40                      45

cct ggg ccc ctg gag cct gag gag ccg aga gct gga ggc agg cct cgg 250
Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg
                      50                      55                      60                      65

cgc cgg agg gac ctg ggc agc cgc cta cag gcc cag cgt cga gcc cag 298
Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln
                      70                      75                      80

cgg gtg gcc tgg gca gaa gca gat gag aac gag gag gaa gct gtc atc 346
Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile
                      85                      90                      95

cta gcc cag gag gag gaa ggt gtc gag aag cca gcg gaa act cac ctg 394

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Leu	Ala	Gln	Glu	Glu	Glu	Gly	Val	Glu	Lys	Pro	Ala	Glu	Thr	His	Leu		
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tcg	ggg	aaa	att	gga	gct	aag	aaa	ctg	cgg	aag	ctg	gag	gag	aaa	caa	442	
Ser	Gly	Lys	Ile	Gly	Ala	Lys	Lys	Leu	Arg	Lys	Leu	Glu	Glu	Lys	Gln		
115						120				125							
gcg	cga	aag	gcc	cag	cgt	gag	gca	gag	gag	gct	gaa	cgt	gag	gag	cgg	490	
Ala	Arg	Lys	Ala	Gln	Arg	Glu	Ala	Glu	Glu	Ala	Glu	Arg	Glu	Glu	Arg		
130				135						140				145			
aaa	cga	ctc	gag	tcc	cag	cgc	gaa	gct	gag	tgg	aag	aag	gag	gag	gag	538	
Lys	Arg	Leu	Glu	Ser	Gln	Arg	Glu	Ala	Glu	Trp	Lys	Lys	Glu	Glu	Glu		
				150				155						160			
cgg	ctt	cgc	ctg	gag	gag	gag	cag	aag	gag	gag	gag	gag	agg	aag	gcc	586	
Arg	Leu	Arg	Leu	Glu	Glu	Glu	Gln	Lys	Glu	Glu	Glu	Glu	Arg	Lys	Ala		
		165						170				175					
cgc	gag	gag	cag	gcc	cag	cgg	gag	cat	gag	gag	tac	ctg	aaa	ctg	aag	634	
Arg	Glu	Glu	Gln	Ala	Gln	Arg	Glu	His	Glu	Glu	Tyr	Leu	Lys	Leu	Lys		
180						185						190					
gag	gcc	ttt	gtg	gtg	gag	gag	gaa	ggc	gta	gga	gag	acc	atg	act	gag	682	
Glu	Ala	Phe	Val	Val	Glu	Glu	Glu	Gly	Val	Gly	Glu	Thr	Met	Thr	Glu		
195						200				205							
gaa	cag	tcc	cag	agc	ttc	ctg	aca	gag	ttc	atc	aac	tac	atc	aag	cag	730	
Glu	Gln	Ser	Gln	Ser	Phe	Leu	Thr	Glu	Phe	Ile	Asn	Tyr	Ile	Lys	Gln		
210				215						220				225			
tcc	aag	gtt	gtg	ctc	ttg	gaa	gac	ctg	gct	tcc	cag	gtg	ggc	cta	cgc	778	
Ser	Lys	Val	Val	Leu	Leu	Glu	Asp	Leu	Ala	Ser	Gln	Val	Gly	Leu	Arg		
				230				235						240			
act	cag	gac	acc	ata	aat	cgc	atc	cag	gac	ctg	ctg	gct	gag	ggg	act	826	
Thr	Gln	Asp	Thr	Ile	Asn	Arg	Ile	Gln	Asp	Leu	Leu	Ala	Glu	Gly	Thr		
		245						250				255					
ata	aca	ggt	gtg	att	gac	gac	cgg	ggc	aag	ttc	atc	tac	ata	acc	cca	874	
Ile	Thr	Gly	Val	Ile	Asp	Asp	Arg	Gly	Lys	Phe	Ile	Tyr	Ile	Thr	Pro		
260						265						270					
gag	gaa	ctg	gcc	gcc	gtg	gcc	aac	ttc	atc	cga	cag	cgg	ggc	cgg	gtg	922	
Glu	Glu	Leu	Ala	Ala	Val	Ala	Asn	Phe	Ile	Arg	Gln	Arg	Gly	Arg	Val		
275						280				285							
tcc	atc	gcc	gag	ctt	gcc	caa	gcc	agc	aac	tcc	ctc	atc	gcc	tgg	ggc	970	
Ser	Ile	Ala	Glu	Leu	Ala	Gln	Ala	Ser	Asn	Ser	Leu	Ile	Ala	Trp	Gly		
290				295						300				305			
cgg	gag	tcc	cct	gcc	caa	gcc	cca	gcc	tga	ccccagtcct	tccctcttgg					1020	
Arg	Glu	Ser	Pro	Ala	Gln	Ala	Pro	Ala	*								
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 <211> 1875
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79)...(666)

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 Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala
 1 5 10

gac cca agc gat ctg gag agc ggc ggg ctg ctg cat gag att ttc acg 159
 Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr
 15 20 25

tcg ccg ctc aac ctg ctg ctg ctt ggc ctc tgc atc ttc ctg ctc tac 207
 Ser Pro Leu Asn Leu Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr
 30 35 40

aag atc gtg cgc ggc gac cag ccg gcg gcc agc ggc gac agc gac gac 255
 Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp
 45 50 55

gac gag ccg ccc cct ctg ccc cgc ctc aag cgg cgc gac ttc acc ccc 303
 Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro
 60 65 70 75

gcc gag ctg cgg cgc ttc gac ggc gtc cag gac ccg cgc ata ctc atg 351
 Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met
 80 85 90

gcc atc aac ggc aag gtg ttc gat gtg acc aaa ggc cgc aaa ttc tac 399
 Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr
 95 100 105

ggg ccc gag ggc ccg tat ggg gtc ttt gct gga aga gat gca tcc agg 447
 Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg
 110 115 120

ggc ctt gcc aca ttt tgc ctg gat aag gaa gca ctg aag gat gag tac 495
 Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr
 125 130 135

gat gac ctt tct gac ctc act gct gcc cag cag gag act ctg agt gac 543
 Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp
 140 145 150 155

tgg gag tct cag ttc act ttc aag tat cat cac gtg ggc aaa ctg ctg 591
 Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His Val Gly Lys Leu Leu
 160 165 170

aag gag ggc gag gag ccc act gtg tac tca gat gag gaa gaa cca aaa 639

Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys
 175 180 185

gat gag agt gcc cgg aaa aat gat taa agcattcagt ggaagtatat 686
 Asp Glu Ser Ala Arg Lys Asn Asp *
 190 195

ctatttttgt attttgcaaa atcatttgta acagtcact ctgtctttaa aacatagtga 746
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 ggtaaaatag tcattgtatt ttcttgtgaa ctgtgtttta tgattttacc tcaaatcaga 1826
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<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 47

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 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu
 1 5 10

gcg ttg gtg gga gcc gtg ctc tac ctc tat ccg gct tcc aga caa gct 158
 Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala
 15 20 25

gca gga att cca ggg att act cca act gaa gaa aaa gat ggt aat ctt 206
 Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 30 35 40 45

cca gat att gtg aat agt gga agt ttg cat gag ttc ctg gtt aat ttg 254
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu
 50 55 60

cat gag aga tat ggg cct gtg gtc tcc ttc tgg ttt ggc agg cgc ctc 302
 His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu

65					70					75						
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		80					85					90				
aat	aag	aca	ttg	gac	cct	ttt	gaa	acc	atg	ctg	aag	tca	tta	tta	agg	398
Asn	Lys	Thr	Leu	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	Ser	Leu	Leu	Arg	
	95					100					105					
tat	caa	tct	ggg	ggg	ggc	agt	gtg	agt	gaa	aac	cac	atg	agg	aaa	aaa	446
Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	His	Met	Arg	Lys	Lys	
110					115					120					125	
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Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	Lys	Ser	Asn	Phe	Ala	Leu	
				130					135					140		
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Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro	
			145					150					155			
gag	acc	cag	cac	gtg	ccc	ctc	agc	cag	cat	atg	ctt	ggg	ttt	gct	atg	590
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Lys	Ser	Val	Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	
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Glu	Val	Ile	Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	
190					195					200					205	
gga	aaa	ggc	ttt	cta	gat	ggg	tca	ctt	gat	aaa	aac	atg	act	cgg	aaa	734
Gly	Lys	Gly	Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	
				210					215					220		
aaa	caa	tat	gaa	gat	gcc	ctc	atg	caa	ctg	gag	tct	gtt	tta	agg	aac	782
Lys	Gln	Tyr	Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	
			225					230					235			
atc	ata	aaa	gaa	cga	aaa	gga	agg	aac	ttc	agt	caa	cat	att	ttc	att	830
Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	
		240					245					250				
gac	tcc	tta	gta	caa	ggg	aac	ctt	aat	gac	caa	cag	atc	cta	gaa	gac	878
Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	
	255					260					265					
agt	atg	ata	ttt	tct	ctg	gcc	agt	tgc	ata	ata	act	gca	aaa	ttg	tgt	926
Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
270					275					280					285	
acc	tgg	gca	atc	tgt	ttt	tta	acc	acc	tct	gaa	gaa	gtt	caa	aaa	aaa	974
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	
				290					295					300		

tta tat gaa gag ata aac caa gtt ttt gga aat ggt cct gtt act cca 1022
 Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val Thr Pro
 305 310 315
 gag aaa att gag cag ctc aga tat tgt cag cat gtg ctt tgt gaa act 1070
 Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu Cys Glu Thr
 320 325 330
 gtt cga act gcc aaa ctg act cca gtt tct gcc cag ctt caa gat att 1118
 Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln Leu Gln Asp Ile
 335 340 345
 gaa gga aaa att gac cga ttt att att cct aga gag acc ctc gtc ctt 1166
 Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg Glu Thr Leu Val Leu
 350 355 360 365
 tat gcc ctt ggt gtg gta ctt cag gat cct aat act tgg cca tct cca 1214
 Tyr Ala Leu Gly Val Val Leu Gln Asp Pro Asn Thr Trp Pro Ser Pro
 370 375 380
 cac aag ttt gat cca gat cgg ttt gat gat gaa tta gta atg aaa act 1262
 His Lys Phe Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr
 385 390 395
 ttt tcc tca ctt gga ttc tca ggc aca cag gag tgt cca gag ttg agg 1310
 Phe Ser Ser Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg
 400 405 410
 ttt gca tat atg gtg acc aca gta ctt ctt agt gta ttg gtg aag aga 1358
 Phe Ala Tyr Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg
 415 420 425
 ctg cac cta ctt tct gtg gag gga cag gtt att gaa aca aag tat gaa 1406
 Leu His Leu Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu
 430 435 440 445
 ctg gta aca tca tca agg gaa gaa gct tgg atc act gtc tca aag aga 1454
 Leu Val Thr Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg
 450 455 460
 tat taa aattttatac atttaaaatc attgttaaatt tgattgagga aacaaccatt 1510
 Tyr *
 taataaaaaat ctatgttgaa tcctttttata aaccagtatc acttttgtaat at 1562

<210> 48

<211> 2030

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (171)...(914)

<400> 48

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 Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly Leu
 215 220 225

tgg gcc ttc atc aca gct gga ggg tcc ctc cga agt att cag cgc agc 896
 Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln Arg Ser
 230 235 240

ctc ttg tgt aag gac tga ctacctggac tgatcgccctg acagatccca 944
 Leu Leu Cys Lys Asp *
 245

cctgcctgtc cactgcccac gactgagccc agccccagcc cgggtccatt gccacattc 1004
 tctgtctcct tctcgtcggc ctacccccact acctccaggg ttttgctttg tccttttgtg 1064
 accgttagtc tctaagcttt accaggagca gcctgggttc agccagtcag tgactggtgg 1124
 gtttgaatct gcacttatcc ccaccacctg gggaccccct tgttgtgtcc aggactcccc 1184
 ctgtgtcagt gctctgctct caccctgccc aagactcacc tcccttcccc tctgcaggcc 1244
 gacggcagga ggacagtcgg gtgatgggtg attctgccct gcgcatcca cccgaggact 1304
 gagggaaacct aggggggacc cctgggcctg gggtgcccctc ctgatgtcct cgccctgtat 1364
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 tccctcaaga ctggacatct tggctttttt ctcaggcctg aggggggaacc attttttgtg 1544
 tgataaatac cctaaactgc ctttttttct tttttgaggt ggggggaggg aggaggtata 1604
 ttggaactct tctaacctcc ttgggctata ttttctctcc tcgagttgct cctcatggct 1664
 gggctcattt cggctccctt ctcttgggtc ccagaccttg ggggaaagga aggaagtgca 1724
 tgtttgggaa ctggcattac tggaactaat ggttttaacc tccttaacca ccagcatccc 1784
 tcctctcccc aagggtgaagt ggaggggtgct gtggtgagct ggccactcca gagctgcagt 1844
 gccactggag gagtacagact accatgacat cgtaggggaag gaggggagat tttttttag 1904
 tttttaattg ggggtgtggga ggggcgggga ggttttctat aaactgtatc attttctgct 1964
 gaggttggag tgtcccatcc ttttaatcaa ggtgattgtg attttgacta ataaaaaaga 2024
 atttgt 2030

<210> 49
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (98)...(439)

<400> 49
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 tccgtcccga gaaggagaa gaggccgaag aggaaac atg aac ttc tat tta ctc 115
 Met Asn Phe Tyr Leu Leu
 1 5

cta gcg agc agc att ctg tgt gcc ttg att gtc ttc tgg aaa tat cgc 163
 Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile Val Phe Trp Lys Tyr Arg
 10 15 20

cgc ttt cag aga aac act ggc gaa atg tca tca aat tca act gct ctt 211
 Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu
 25 30 35

gca cta gtg aga ccc tct tct tct ggg tta att aac agc aat aca gac 259

Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp
 40 45 50

aac aat ctt gca gtc tac gac ctc tct cgg gat att tta aat aat ttc 307
 Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe
 55 60 65 70

cca cac tca ata gcc agg cag aag cga ata ttg gta aac ctc agt atg 355
 Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met
 75 80 85

gtg gaa aac aag ctg gtt gaa ctg gaa cat act cta ctt agc aag ggt 403
 Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly
 90 95 100

ttc aga ggt cca tca cct cac cgg aaa tcc acc taa aagcgtacag 449
 Phe Arg Gly Pro Ser Pro His Arg Lys Ser Thr *

105 110

gatgtaatgc cagtgggtgga aatcattaaa gacactttga gtag 493

<210> 50
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (288)...(1385)

<400> 50
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 aattaaccat gggaagggtc agcaccagcc accagcccct taggtgagga ctctgcctgg 120
 ggctctgctg atgggtccga atcatggagc tgcagagagc tcctccagcc tggagacgtt 180
 cttggtgaaa gctgtggtct aactccaccg gctcttctctg cacattgtat tcaagagggg 240
 tgcctgcccc cgctgactca ggagctccgg tgctgcagcc gccacga atg ggg agg 296
 Met Gly Arg
 1

tgg gcc ctc gat gtg gcc ttt ttg tgg aag gcg gtg ttg acc ctg ggg 344
 Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly
 5 10 15

ctg gtg ctt ctc tac tac tgc ttc tcc atc ggc atc acc ttc tac aac 392
 Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn
 20 25 30 35

aag tgg ctg aca aag agc ttc cat ttc ccc ctc ttc atg acg atg ctg 440
 Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu
 40 45 50

cac ctg gcc gtg atc ttc ctc ttc tcc gcc ctg tcc agg gcg ctg gtt 488
 His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg Ala Leu Val
 55 60 65

cag tgc tcc agc cac agg gcc cgt gtg gtg ctg agc tgg gcc gac tac 536
 Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp Ala Asp Tyr

70					75					80						
ctc	aga	aga	gtg	gct	ccc	aca	gct	ctg	gcg	acg	gcg	ctt	gac	gtg	ggc	584
Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	Asp	Val	Gly	
	85						90				95					
ttg	tcc	aac	tgg	agc	ttc	ctg	tat	gtc	acc	gtc	tcg	ctg	tac	aca	atg	632
Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	Tyr	Thr	Met	
100					105					110					115	
acc	aaa	tcc	tca	gct	gtc	ctc	ttc	atc	ttg	atc	ttc	tct	ctg	atc	ttc	680
Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Ile	Phe	
				120					125					130		
aag	ctg	gag	gag	ctg	cgc	gcg	gca	ctg	gtc	ctg	gtg	gtc	ctc	ctc	atc	728
Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	Leu	Leu	Ile	
		135						140					145			
gcc	ggg	ggt	ctc	ttc	atg	ttc	acc	tac	aag	tcc	aca	cag	ttc	aac	gtg	776
Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	Phe	Asn	Val	
	150						155					160				
gag	ggc	ttc	gcc	ttg	gtg	ctg	ggg	gcc	tcg	ttc	atc	ggt	ggc	att	cgc	824
Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	Gly	Ile	Arg	
165						170				175						
ttg	acc	ctc	acc	cag	atg	ctc	ctg	cag	aag	gct	gaa	ctc	ggc	ctc	cag	872
Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	Gly	Leu	Gln	
180					185					190					195	
aat	ccc	atc	gac	acc	atg	ttc	cac	ctg	cag	cca	ctc	atg	ttc	ctg	ggg	920
Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	Phe	Leu	Gly	
				200					205					210		
ctc	ttc	cct	ctc	ttt	gct	gta	ttt	gaa	ggt	ctc	cat	ttg	tcc	aca	tct	968
Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	Ser	Thr	Ser	
			215					220					225			
gag	aaa	atc	ttc	cgt	ttc	cag	gac	aca	ggg	ctg	ctc	ctg	cgg	gta	ctt	1016
Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	Arg	Val	Leu	
	230						235					240				
ggg	agc	ctc	ttc	ctt	ggc	ggg	att	ctc	gcc	ttt	ggt	ttg	ggc	ttc	tct	1064
Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu	Gly	Phe	Ser	
	245					250				255						
gag	ttc	ctc	ctg	gtc	tcc	aga	acc	tcc	agc	ctc	act	ctc	tcc	att	gcc	1112
Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu	Ser	Ile	Ala	
260					265					270					275	
ggc	att	ttt	aag	gaa	gtc	tgc	act	ttg	ctg	ttg	gca	gct	cat	ctg	ctg	1160
Gly	Ile	Phe	Lys	Glu	Val	Cys	Thr	Leu	Leu	Leu	Ala	Ala	His	Leu	Leu	
				280					285					290		
ggc	gat	cag	atc	agc	ctc	ctg	aac	tgg	ctg	ggc	ttc	gcc	ctc	tgc	ctc	1208
Gly	Asp	Gln	Ile	Ser	Leu	Leu	Asn	Trp	Leu	Gly	Phe	Ala	Leu	Cys	Leu	
			295					300					305			

tgc	gga	ata	tcc	ctc	cac	gtt	gcc	ctc	aaa	gcc	ctg	cat	tcc	aga	ggt	1256
Ser	Gly	Ile	Ser	Leu	His	Val	Ala	Leu	Lys	Ala	Leu	His	Ser	Arg	Gly	
		310					315					320				

gat ggt ggc ccc aag gcc ttg aag ggg ctg ggc tcc agc ccc gac ctg 1304
Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu
325 330 335

gag ctg ctg ctc cgg agc agc cag cgg gag gaa ggt gac aat gag gag 1352
Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu
340 345 350 355

gag gag tac ttt gtg gcc cag ggg cag cag tga ccagccaggg caaatggctt 1405
Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln *
360 365

agaagcaggc	cactccccag	cctgctgcc	gcactcactg	tgtccaagcc	gccagggctc	1465
atcatggtag	ctgggagctg	tggacgggag	tcaccagggtg	gtggggccaa	gccaggggact	1525
catgactttt	gcccctccct	tcagagcctg	gtcacacaag	gggcgagcac	caggccagcc	1585
tgggactggc	cagagctggg	cccaagctgc	gctggaatcg	cagcaggaga	ggggagtggg	1645
ctggttcttc	ccaccacttc	ccaggctctg	acagccgaga	ctcatttcca	aggcacagca	1705
gctttctaaa	gggactgagt	ttggactggg	ttttggacct	ccagggggctg	gagcttcatc	1765
acctgggcag	tgtctttttc	cagagagcag	gtttctttat	agtttgga	taaatggttc	1825
acggtccact	ggcgccttg	tgttgctgga	gacgtggggg	cagggagggg	acagtgtggg	1885
cctggcctct	cctttccttt	cctgcctgg	agccttcttc	aaatgtctgg	tcttaagcca	1945
ggcctccttc	attttctcgc	tctgtttaga	acaccagtc	cctcccagt	ggggccccac	2005
tgcacctgct	ggcaggaat	aaatgaatgt	ttactgaqt			2044

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<210> 51
<211> 1043
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (157) ... (837)
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<400> 51
attagcataa cccttcctca ggaagagtga gattttatat ttgacaataa agtggttagac 60
tccattttcta aataccagac ttcaaaagat aagggttcaaa agtggttataa gaagatattc 120
ctttttttgt cctagagaac ttatttttct gtgaaa atg cct acc aca aag aag 174
                               Met Pro Thr Thr Lys Lys
                               1             5

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aca ttg atg ttc tta tca agc ttt ttc acc agc ctt ggg tcc ttc att 22
Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile

10 15 20

gta att tgc tct att ctt ggg aca caa gca tgg atc acc agt aca att 270
Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile
25 30 35

gct gtt aga gac tct gct tca aat ggg agc att ttc atc act tac gga 318
Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly
40 45 50

```

ctt ttt cgt ggg gag agt agt gaa gaa ttg agt cac gga ctt gca gaa 366
Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu
55 60 65 70

cca aag aaa aag ttt gca gtt tta gag ata ctg aat aat tct tcc caa 414
Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln
75 80 85

aaa act ctg cat tcg gtg act atc ctg ttc ctg gtc ctg agt ttg atc 462
Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile
90 95 100

acg tcg ctg ctg agc tct ggg ttt acc ttc tac aac agc atc agc aac 510
Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn
105 110 115

cct tac cag aca ttc ctg ggg ccg acg ggg gtg tac acc tgg aac ggg 558
Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly
120 125 130

ctc ggt gca tcc ttc gtt ttt gtg acc atg ata ctg ttt gtg gcg aac 606
Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn
135 140 145 150

acg cag tcc aac caa ctc tcc gaa gag ttg ttc caa atg ctt tac ccg 654
Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro
155 160 165

gca acc acc agt aaa gga acg acc cac agt tac gga tac tcg ttc tgg 702
Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp
170 175 180

ctc ata ctg ctc gtc att ctt cta aat ata gtc act gta acc atc atc 750
Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile
185 190 195

att ttc tac cag aag gcc aga tac cag cgg aag cag gag cag aga aag 798
Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys
200 205 210

cca atg gaa tat gct cca agg gac gga att tta ttc tga attctctttc 847
Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe *
215 220 225

atctcattttt ggcgttgcat ctattgtaca tcagccctga gtagtaactg gttagcttct 907
ctggacaatt cagcatggta acgtgactgt catctgtgac agcattttgtg tttcatgaca 967
ctgtgttctt cattgatgct gtactcctga aaatttttcc cacaagggtg gggaaatgaa 1027
tgggaaatgt cgctgg 1043

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<210> 52

<211> 971

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29)...(418)

<400> 52

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agacagcggc gggcgcagga cgtgcact atg gct cgg ggc tcg ctg cgc cgg 52
                               Met Ala Arg Gly Ser Leu Arg Arg
                               1                     5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 100
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
   10                     15                     20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 148
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
   25                     30                     35                     40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 196
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
                     45                     50                     55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 244
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
                     60                     65                     70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 292
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
                     75                     80                     85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 340
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
   90                     95                     100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 388
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
  105                     110                     115                     120

ggc tgc cca gct gtg gcg ctg atc cag tga caatgtgccc cctgccaccg 438
Gly Cys Pro Ala Val Ala Leu Ile Gln *
                     125

```

```

gggctcgccc actcatcatt cattcatcca ttctagagcc agtctctgcc tcccagacgc 498
ggcgggagcc aagctcctcc aaccacaagg ggggtggggg gcggtgaatc acctctgagg 558
cctgggcccc ggggttcagg gaaccttcca aggtgtctgg ttgccctgcc tctggctcca 618
gaacagaaaag ggagcctcac gctggctcac acaaaacagc tgacactgac taaggaactg 678
cagcatttgc acaggggagg ggggtgccct ccttcctaga ggccctgggg gccaggctga 738
cttggggggc agacttgaca ctaggcccca ctcaactcaga tgtcctgaaa ttccaccacg 798
ggggtcaccc tgggggggta gggacctatt tttaacacta gggggctggc ccactaggag 858
ggctggccct aagatacaga ccccccaac tccccaaagc ggggaggaga tatttatttt 918
ggggagagtt tggaggggag ggagaattta ttaataaaag aatctttaac ttt 971

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<210> 53

<211> 695

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73)...(564)

<400> 53

aagattttcag ctgcgggacg gtcaggggag acctccaggc gcaggggaagg acggccaggg 60
 tgacacggaa gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggc 111
 Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
 1 5 10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc 159
 Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
 15 20 25

ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg 207
 Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
 30 35 40 45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca 255
 Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
 50 55 60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc 303
 Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
 65 70 75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg 351
 Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
 80 85 90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg ggc tct gag gac aaa 399
 Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
 95 100 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg 447
 Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg
 110 115 120 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct 495
 Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala
 130 135 140

ggt gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc 543
 Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser
 145 150 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg 594
 Lys Ala Leu Pro Arg Ser *
 160

accgctgccg gtggaacca gtggaagacc ccagcccca gggagaggac cccgttctat 654
 cccagccat gataataaag ctgctctccc agctgcctct c 695

<210> 54

<211> 1914

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (80)...(661)

<400> 54

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 ccccgcgccg cccgtcaac atg atc cgc tgc ggc ctg gcc tgc gag cgc tgc 112
 Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys
 1 5 10

cgc tgg atc ctg ccc ctg ctc cta ctc agc gcc atc gcc ttc gac atc 160
 Arg Trp Ile Leu Pro Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile
 15 20 25

atc gcg ctg gcc ggc cgc ggc tgg ttg cag tct agc gac cac ggc cag 208
 Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln
 30 35 40

acg tcc tcg ctg tgg tgg aaa tgc tcc caa gag ggc ggc ggc agc ggg 256
 Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly
 45 50 55

tcc tac gag gag ggc tgt cag agc ctc atg gag tac gcg tgg ggt aga 304
 Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg
 60 65 70 75

gca gcg gct gcc atg ctc ttc tgt ggc ttc atc atc ctg gtg atc tgt 352
 Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys
 80 85 90

ttc atc ctc tcc ttc ttc gcc ctc tgt gga ccc cag atg ctt gtc ttc 400
 Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe
 95 100 105

ctg aga gtg att gga ggt ctc ctt gcc ttg gct gct gtg ttc cag atc 448
 Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile
 110 115 120

atc tcc ctg gta att tac ccc gtg aag tac acc cag acc ttc acc ctt 496
 Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu
 125 130 135

cat gcc aac cgt gct gtc act tac atc tat aac tgg gcc tac ggc ttt 544
 His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe
 140 145 150 155

ggg tgg gca gcc acg att atc ctg atc ggc tgt gcc ttc ttc ttc tgc 592
 Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys
 160 165 170

tgc ctc ccc aac tac gaa gat gac ctt ctg ggc aat gcc aag ccc agg 640
 Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg
 175 180 185

tac ttc tac aca tct gcc taa cttgggaatg aatgtgggag aaaatcgctg 691
 Tyr Phe Tyr Thr Ser Ala *
 190

ctgctgagat ggactccaga agaagaaact gtttctccag gcgactttga acccattttt 751
 tggcagtgtt catattatta aactagtcaa ataagctaaa ataatttggg agaaaaatatt 811

2mb
B17
Cont'd

Q2
cont

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tttcccaata	aaccaggtat	tct				1914
